Amendments to the Specification

Please replace the paragraph beginning on page 46 at line 21 and ending at page 47, line 3 with the following paragraph:

It should be appreciated that in the above table 2, an indicated gene means the gene and all currently known variants thereof, including the different mRNA transcripts that the gene and its variants can give rise to, and any further gene variants which may be elucidated. In general, however, such variants will have significant sequence identity to a sequence of table 2 above, e.g. a variant will have at least about 70 percent sequence identity to a sequence of the above table 2, more typically at least about 75, 80, 85, 90, 95, 97, 98 or 99 percent sequence identity to a sequence of the above table 2. Sequence identity of a variant can be determined by any of a number of standard techniques such as a BLAST program ~~http://www.ncbi.nlm.nih.gov/blast/~~ available on the world wide web at ncbi.nlm.gov/blast~~)~~.

Please replace the paragraph beginning on page 47 at line 5 with the following paragraph:

Sequences for the genes listed in Table 2 can be found in GenBank available on the world wide web at ncbi.nlm.gov ~~(http://www.ncbi.nlm.nih.gov/)~~. The gene sequences may be genomic, cDNA or mRNA sequences. Preferred sequences are viral genes containing the complete coding region and 5' untranslated sequences that are involved in viral replication.

Please replace the paragraph beginning on page 51 at line 5 with the following paragraph:

It should be appreciated that in the above table 5 and 6, an indicated gene means the gene and all currently known variants thereof, including the different mRNA transcripts that the gene and its variants can give rise to, and any further gene variants which may be elucidated. In general, however, such variants will have significant sequence identity to a sequence of table 5 and 6 above, e.g. a variant will have at least about 70 percent sequence identity to a sequence of the above table 5 and 6, more typically at least about 75, 80, 85, 90, 95, 97, 98 or 99 percent sequence identity to a sequence of the above table 5 and 6. Sequence identity of a variant can be determined by any of a number of standard techniques such as a BLAST program ~~http://www.ncbi.nlm.nih.gov/blast/~~ available on the world wide web at ncbi.nlm.gov/blast~~)~~.

Please replace the paragraph beginning on page 51 at line 16 with the following paragraph:

Sequences for the genes listed in Table 5 and 6 can be found in GenBank available on the world wide web at ncbi.nlm.gov ~~(http://www.ncbi.nlm.nih.gov/)~~. The gene sequences may be genomic, cDNA or mRNA sequences. Preferred sequences are viral genes containing the complete coding region and 5' untranslated sequences that are involved in viral replication.

Please replace the paragraph beginning on page 58 at line 19 and continuing to page 59 with the following paragraph:

Sequence similarity searches can be performed manually or by using several available computer programs known to those skilled in the art. Preferably, Blast and Smith-Waterman algorithms, which are available and known to those skilled in the art, and the like can be used. Blast is NCBI's sequence similarity search tool designed to support analysis of nucleotide and protein sequence databases. Blast can be accessed through the world wide web of the Internet, at, for example, ncbi.nlm.nih.gov/BLAST/. The GCG Package provides a local version of Blast that can be used either with public domain databases or with any locally available searchable database. GCG Package v9.0 is a commercially available software package that contains over 100 interrelated software programs that enables analysis of sequences by editing, mapping, comparing and aligning them. Other programs included in the GCG Package include, for example, programs which facilitate RNA secondary structure predictions, nucleic acid fragment assembly, and evolutionary analysis. In addition, the most prominent genetic databases (GenBank, EMBL, PIR, and SWISS-PROT) are distributed along with the GCG Package and are fully accessible with the database searching and manipulation programs. GCG can be accessed through the Internet at, for example, on the world wide web at gcg.com~~http://www.gcg.com/~~. Fetch is a tool available in GCG that can get annotated GenBank records based on accession numbers and is similar to Entrez. Another sequence similarity search can be performed with GeneWorld and GeneThesaurus from Pangea. GeneWorld 2.5 is an automated, flexible, high-throughput application for analysis of polynucleotide and protein sequences. GeneWorld allows for automatic analysis and annotations of sequences. Like GCG, GeneWorld incorporates several tools for homology searching, gene finding, multiple sequence

alignment, secondary structure prediction, and motif identification. GeneThesaurus 1.0 ™ is a sequence and annotation data subscription service providing information from multiple sources, providing a relational data model for public and local data.

Please replace the paragraph beginning on page 63 at line 4 with the following paragraph:

Sequences for the genes listed in Tables 7 - 10 can be found in GenBank available on the world wide web at ncbi.nlm.gov ~~(http://www.ncbi.nlm.nih.gov/)~~. The gene sequences may be genomic, cDNA or mRNA sequences. Preferred sequences are mammalian genes comprising the complete coding region and 5' untranslated sequences. Particularly preferred are human cDNA sequences.

Please replace the paragraph beginning on page 29 at line 26 and continuing to page 30 with the following paragraph:

FIG. 1 is a schematic illustration showing possible antigene lock conformations and target mechanism of antigene lock target binding. Antigene locks, shown in the top of the figure, ~~(blue)~~ are shown in equilibrium between the native closed conformation (top left) and the open active conformation (top right). Note that the terminal bases of both arms are mispaired with the backbone. The gene target, shown in the middle of the figure, ~~(red)~~ may also be in equilibrium between double-stranded and denatured forms (middle). The antigene lock interacts with the denatured target (bottom right). Note the homology between the arms (including the terminal bases) and the target, while the mispairing between the lock and the target is in the backbone. The proposed structure of bound and ligated antigene lock is shown (bottom left). Since the backbone and combined arm lengths are 40 bases each, the antigene lock should be intertwined four times with each strand of the target DNA before being ligated.

Please replace the paragraph beginning on page 30 at line 6 with the following paragraph:

FIG. 2A-2D show that the antigene lock structures bind specifically to their targets, and in the presence of DNA ligase, inhibit DNA synthesis in-vitro. FIG. 2A is a schematic of a plasmid showing the position of the pUC19 polylinker antigene lock ~~(orange)~~ on the target on the pUC19

plasmid (not drawn to scale). FIG. 2B, is a gel showing an Electrophoretic Mobility Shift Assay (EMSA) which demonstrates that the sequence specific antigene lock reacts with only the plasmid bearing the target sequence spontaneously at physiologic temperature. .sup.32P-labeled pUC19 antigene lock was incubated with pUC19 (lane 1), alone (lane 2), with pSG5 plasmid (lane 3) or pUC19-.DELTA.PL (lane 4). FIG. 2C is a gel showing antigene lock binding was increased in the presence of DNA ligase. .sup.32P-labeled pUC19 antigene lock was incubated alone (lane 1), with pUC19 (lane 2) or with pUC19 and DNA ligase. FIG. 2D print out showing that DNA synthesis was arrested by the presence of the antigene lock during cycle sequencing. The antigene lock was mixed with pUC19, heated denatured, incubated with or without DNA ligase and cycle sequenced with either sequencing primer A or B.

Please replace the paragraph beginning on page 32 at line 10 with the following paragraph:

FIGS. 6A-6C show that gene specific antigene locks can kill human cervical cancer cells. FIG. 6A is a schematic illustration showing the position of the antigene locks ~~(red)~~ on their targets on the alu repeat and the HPV-16 E7 oncogene (not drawn to scale). FIG. 6B is a bar graph showing gene specific alu antigene lock specifically kills human cervical cancer cells. Reduction in colony count was monitored after transfection with the alu sequence specific or control alu antigene locks in three human cervical cancer or A9 mouse cell lines. Bars represent the means of 3 independent experiments and error bars, standard error of the mean. p values were calculated using a paired t-test. FIG. 6C is a bar graph showing gene specific E7 antigene lock selectively kills human cervical cancer cells, CaSki and C33A/E7, which contain the E7 gene target. Reduction of in colony count after transfection with the E7 sequence-specific or control E7 antigene locks was determined in the three cervical cancer cell lines.

Please replace the paragraph beginning on page 32 at line 23 with the following paragraph:
FIG. 7A-7F shows the production of white colonies when 8036/+6 cells are transformed with either lacZ or proA anti-gene locks. FIG. 7A is a schematic illustration showing the position of the anti-gene locks ~~(orange)~~ on their targets on the lacZ and proA genes (not drawn to scale). FIGS. 7B-7E shows the production of white colonies (arrows) when 8036/+6 cells were transformed with either lacZ or proA anti-gene locks. Phosphorylated lacZ or proA anti-gene locks (FIGS. 7C and 7E) or lacZ or proA control anti-gene locks (FIGS. 7B and 7D) were co-

transformed with pSG5 plasmid, at a molar ratio of 9000:1 (anti-gene lock: plasmid), into competent E. coli 8036/+6 cells, and plated out on Xgal plates containing exogenous proline. Note the absence of sectored colonies. FIG. 7F is a bar graph comparing the production of white colonies in 8036/+6 after transformation with the sequence specific lacZ and proA anti-gene locks and their controls. The data represents the means of 4 independent experiments and error bars, standard error of the mean. p values were calculated using a paired t-test.